POSTER SUBMISSIONS

Take the opportunity to discuss cutting edge research during the poster presentation slots on day one!

Odd Numbers: 13.00 – 14:30, Foyer Level 2
Even Numbers: 16.50 – 17.50, Foyer Level 2

1.	**Diagnostic Innovation and Livestock: Towards more effective and sustainable applications of antibiotics in livestock farming**
	Katie Adam *et al.,* University of Edinburgh
2.	**In vitro comparison of oxazolidinones shows superior efficacy of tedizolid in comparison to linezolid against staphylococci**
	Muna Aleryan *et al.,* Glasgow Caledonian University
3.	**An Investigation of 5-Fluorouracil Resistance in Kinetoplast Parasites**
	Ibrahim Alfayez *et al.,* University of Glasgow
4.	**Site-directed mutagenesis of specific amino acid residues supports the model of conductance of pentamidine through the TbAQP2 channel**
	Ali Alghamdi *et al.,* University of Glasgow
5.	**Essentiality of pSCL4, a Giant Linear Plasmid of Streptomyces clavuligerus**
	Lis Algora *et al.,* University of Strathclyde
6.	**Multidrug Resistant Acinetobacter baumannii: An Emerging Health Threat in Aseer Region, Kingdom of Saudi Arabia**
	Mohammed Almaghrabi *et al.,* King Khalid University
7.	**Developing protein antibiotics for treatment of AMR Pseudomonas aeruginosa**
	Madhuri Barge *et al.,* University of Glasgow
8.	**Novel Antimicrobial Mechanisms in Phagocytic Cells**
	Massimiliano Baldassarre *et al.,* University of Aberdeen
9.	**Development Of Streptomyces To Utilise Sustainable Feedstock In Fermentations**
	Anna Birke *et al.,* University of Strathclyde
10.	**Using individual-based mathematical models to study antibiotic resistance**
	Ruth Bowness *et al.,* University of St Andrews
11.	**Detection of AMR and co-selectors in drinking water**
	Helen Bridle, University of Heriot Watt
12.	**Understanding the chemical warfare of actinomycetes across taxonomic and phylogenetic boundaries for accelerated antibiotic discovery**
	Laia Castano Espriu *et al.,* University of Strathclyde
13.	**Longitude Prize**
	Paul Chapman, Marks and Clerk
14.	**Role of Implant Nanoroughness and Bioactive coating on Osseointegration and Bacterial Growth**
	Laila Damiati *et al.,* University of Glasgow
15.	**Novel Streptomyces compound discovery by LC/MS guided screening of growth conditions**
	Christine Edwards *et al.,* Robert Gordon University
16.	**Mutants versus cations: variable effects on biofilm formation by Pseudomonas aeruginosa PA14**
	Georgios Efthimiou *et al.,* University of Strathclyde

17.	**Evaluation of greater wax moth larvae, Galleria mellonella, as a novel in vivo model for non-tuberculosis Mycobacteria infections and antibiotic treatments**
	Frances Entwistle, University of St Andrews
18.	**Assessing the impact of changes in national antibiotic use in Scotland on Gram-negative resistance using the NHS Scotland Infection Intelligence Platform**
	Eilidh Fletcher *et al.,* National Health Service
19.	**Characterisation of risk factors associated with antibiotic resistance in urinary isolates in the community: an exemplar of NHS Scotland's Infection Intelligence Platform**
	Eilidh Fletcher *et al.,* National Health Service
20.	**Whole Genome Sequencing (WGS) of Enhanced Surveillance Escherichia coli and Staphylococcus aureus Bacteraemias (ECB and SAB) to investigate the development of AMR in Scottish National Health Service (NHS) health boards**
	Stephen Fox *et al.,* University of Glasgow
21.	**How does Staphylococcus aureus adapt, survive and cause infection? A molecular approach for the identification of novel antibiotic targets.**
	Andreas Haag, University of Glasgow
22.	**Genomic Mining of Thermophilic Actinobacteria for Novel Antibiotics**
	Gillian Halket *et al.,* University of Strathclyde
23.	**Rapid phenotypic susceptibility testing of bacteria: SLIC by name and slick by nature**
	Robert Hammond *et al.,* University of St Andrews
24.	**Investigations into terpenoids action on the Shigella sonnei protein, DsbA by enzymatic kinetic assay**
	Thaer Hasan *et al.,* University of Strathclyde
25.	**Antimicrobial resistance (AMR): which measures should we use?**
	Roger Humphry *et al.,* SRUC
26.	**Synthetic Phage-inducible Chromosomal Islands, the Trojan Horse against AMR.**
	Rodrigo Ibarra-Chavez *et al.,* University of Glasgow
27.	**Cephalosporin resistance levels can be significantly influenced in members of a novel E. coli multidrug-resistant, ESBL-producing clade.**
	Marta J Piotrowska *et al.,* University of Heriot Watt
28.	**Micro technologies for fast bacteria separation and purification from clinical samples**
	Melanie Jimenez *et al.,* University of Glasgow
29.	**The Use of Differentiated Airway Epithelial Cell Cultures for Assessing Antibiotic Transport and Activity within the Bovine Respiratory Tract**
	Claire Jones *et al.,* University of Glasgow
30.	**Characterization of virulence factors in Leishmania mexicana by comparative Omics approaches**
	Abdulbaset Kabli *et al.,* University of Glasgow
31.	**Antimicrobial resistance genes: environmental impacts across landscapes in NE England and Scotland**
	Charles Knapp *et al.,* University of Strathclyde
32.	**The dynamic picture of antimicrobial resistances in Campylobacter spp isolated from different host reservoirs in Scotland.**
	Bruno Lopes *et al.,* University of Aberdeen
33.	**A novel mecC allotype, mecC3, in a new staphylococcal species, Staphylococcus caeli**
	Alison MacFadyen *et al.,* University of Edinburgh
34.	**Exploring Aurodox, A potential anti-virulence compound for the treatment of Escherichia coli infections of the gut.**
	Rebecca McHugh *et al.,* University of Strathclyde

35.	**Evaluation of antimicrobial resistance and biofilm formation of MRSA isolates from companion animals in Scotland**
	Katarina Oravcova *et al.,* University of Glasgow
36.	**What are the trends in antimicrobial resistance patterns in bacteria isolated from companion animals in Scotland?**
	Katarina Oravcova *et al.,* University of Glasgow
37.	**The distribution of antibiotic resistance genes in fresh water in Scotland**
	Eulyn Pagaling *et al.,* The James Hutton Institute
38.	**Antibody based biologics for treating bacterial and fungal infections**
	Soumya Palliyil Soman *et al.,* University of Aberdeen
39.	**Applying the Mesolens to Microbiology - Visualising Biofilm Architecture and Substructure**
	Liam Rooney *et al.,* University of Strathclyde
40.	**FBI Probe to Investigate Ivermectin Resistance in Nematodes**
	Stuart Ruddell *et al.,* University of Glasgow
41.	**Are antimicrobial stewardship and sepsis awareness competing goals? A quantitative content analysis of UK national newspapers**
	Lynne Rush *et al.,* University of Glasgow
42.	**Characterisation of Inducible Antibiotic Production by Streptomycetes Isolated From Hyper-arid Environments**
	Tiago Santos *et al.,* University of Strathclyde
43.	**Analysis of the microbiome of wastewater and the prevalence of resistant Escherichia coli.**
	Janice Spencer *et al.,* Glasgow Caledonian University
44.	**Bacterial Antibiotic Response in Micro-Environments**
	Daniel Taylor *et al.,* University of Edinburgh
45.	**Co-selection of Antibiotic Resistance caused by a Legacy of PTE Pollution in Gram-Negative Bacteria**
	Rebecca Toner *et al.,* University of Strathclyde
46.	**Estimates of antimicrobial usage on Scottish beef and dairy farms.**
	Sue Tongue *et al.,* SRUC
47.	**Osteogenic and bactericidal properties of hydrothermal titania nanowires on titanium substrates**
	Monica P Tsimbouri *et al.,* University of Glasgow
48.	**Heavy Metal Inducible Antimicrobial Activity of Streptomyces spp. Isolated from the Leadhills and Wanlockhead Lead Mines in Scotland.**
	Nick Tucker *et al.,* University of Strathclyde
49.	**Genes of past, present and future: does legacy pollution contribute to antibiotic resistance in industrialised estuaries?**
	Fiona Henriquez *et al.,* University of the West of Scotland

1. Diagnostic Innovation and Livestock: Towards more effective and sustainable applications of antibiotics in livestock farming

Authors: K. Adam, A. Bruce, G. Banda, V. Mugittu, J. Tait.
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Abstract:

Rapid diagnostics have potential to address the challenge of antimicrobial resistance (AMR) in humans and animals. However, successful development and application of novel diagnostic tools requires both scientific innovation and understanding of relevant social, political and economic factors, including regulation.

The Diagnostic Innovation and Livestock (DIAL) project aims to facilitate the development of novel, rapid diagnostic tests to support decisions around antimicrobial use in livestock in the UK and Tanzania. This is an interdisciplinary investigation bringing together social, veterinary and innovation sciences. Using an innovation systems approach, we aim to identify barriers and enablers to diagnostic innovation, assess the regulatory support required and understand potential markets for rapid AMR diagnostics in livestock.

Our research is based on semi-structured interviews and workshops with diagnostic developers, regulators and laboratories. Data will be analysed qualitatively, using the Strategic Planning for Advanced Technology Innovation Systems (STRATIS) framework.

This approach requires collaboration between social and life scientists and will create interdisciplinary networks for the development of practical strategies to optimise antimicrobial use in livestock. We are now recruiting participants and seeking to raise awareness of the project among stakeholders from industry, research and policy.

Notes:

2. In vitro comparison of oxazolidinones shows superior efficacy of tedizolid in comparison to linezolid against staphylococci

Authors: Muna Aleryan1, Brian Jones2, Curtis Gemmell3 and Sue Lang1
Affiliation: [1] Department of Life Sciences, Glasgow Caledonian University, UK; [2] Microbiology Department, Glasgow Royal Infirmary, UK; [3] University of Strathclyde, UK
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Abstract:

Tedizolid is a second-generation oxazolidinone approved for the treatment of acute bacterial skin and skin-structure infections. The study aim was to compare the *in vitro* efficacy of the tedizolid and linezolid with vancomycin against planktonic and biofilm-associated staphylococci.

Clinical isolates of *Staphylococcus aureus* strains (26 MSSA, 27 MRSA) and *S.epidermidis* (12), including three linezolid-resistant (Lnz^R) isolates, were tested for susceptibility to tedizolid, linezolid and vancomycin using EUCAST guidelines. Susceptibility of biofilm-associated cells was assessed using a 96-well plate-resazurin assay.

Compared to linezolid, tedizolid MICs were up to 8-fold lower. The Lnz^R-*cfr*+ isolates remained fully susceptible to tedizolid, whilst the Lnz^R-cfr+/G2576T and Lnz^R-G2576T isolates presented MICs up to 16x greater than linezolid susceptible strains. Tedizolid at 10xMIC displayed greater efficacy than 10xMIC linezolid against pre-formed biofilms, reducing the biofilm by 60% and 42% of the untreated control, respectively. Tedizolid (10xMIC) activity against biofilms formed by Lnz^R-*cfr*+ strains was comparable to the reduction achieved with linezolid though achieved using tedizolid at a concentration 8-fold lower.

The increased activity of tedizolid compared to linezolid achieved using lower concentrations against both planktonic and biofilm-associated cells, including *cfr*+ multidrug resistant strains, offers a realistic lower dose alternative agent in the treatment of staphylococcal infections.

Notes:

3. An Investigation of 5-Fluorouracil Resistance in Kinetoplast Parasites

Authors: Ibrahim Alfayez, Khalid Alzahrani, Juma Ali and Harry de Koning
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Abstract:

Kinetoplastid parasites are a widespread group of flagellated protozoan pathogens and the defining feature of these parasites is the presence of a large mitochondrial DNA region known as the 'kinetoplast'. The most common human diseases caused by kinetoplastid parasites are: 1) African trypanosomes (African sleeping sickness), 2) *Leishmania* species (leishmaniasis) and 3) *Trypanosoma cruzi* (Chagas' disease). The two types of nucleotides in the cell are purine and pyrimidine which have a very significant role in nucleic acid synthesis (DNA and RNA) and the metabolism of prokaryotic and eukaryotic cells. Kinetoplastid parasites are capable of salvage as well as synthesis of pyrimidine nucleotides. Kinetoplastid protozoa express many such membrane transport proteins which enable them to take up nutrients, efflux metabolites, regulate physiological concentrations, translocate various molecules, and import or export drugs. Resistance to 5-fluorouracil (5-FU) was generated in both*T. b. brucei*BSF s427- wild type and*Leishmania mexicana*promastigotes, yielding clonal lines Tbb-5FURes and Lmex-5FURes, respectively. The gene family encoding pyrimidine nucleobase transporters in kinetoplast parasites has not yet been discovered. We try to identify these using the antimetabolite 5-FU as a probe. Previous work in our laboratories (RNA-seq and RIT-seq) analyses of 5-FU resistant cell lines has identified candidate genes for pyrimidine transporters, including genes annotated as cation transporters (*Tbb-CATs*), fatty acid desaturase (*Tbb-FAD* and *Lmex-FAD*) and glucose transporters (*2A*, *1B* and *1E*). Apart from some glucose transporters, none of these potential transport genes have been previously characterised in protozoa and as such they are of interest in their own right as well. The main aim of this study therefore is to identify the gene(s) encoding the protozoan transporters of pyrimidines, particularly uracil, and assess candidate genes that may be involved in transport of, or sensitivity to, 5-FU. For this we will use reverse genetics approaches such as knockout constructs, targeted RNAi, and overexpression of the target genes. We determined the sensitivity of the 5-FU and 6- Azauracil (6-AU) in a sKO of *Tbb-CATs* and *T. b. brucei 427 WT* with the use of alamar blue drug sensitivity assay, and found no significant difference. We were unable to make a full double knockout for the CATs, as this led to the death of the cells, showing that their function is essential for the growth of BSF *T. b. brucei* in vitro. Also, the effect of increased gene expression of *Tbb-FAD* in Tbb-5FURes and *Lmex-FAD* in Lmex-5FURes on 5-FU and 6-AU sensitivities were analysed using the alamar blue assay. Results showed no significant differences in the EC_{50} values of 5-FU and 6-AU between the overexpressing cell lines and the control lines. Efforts to identify the pyrimidine transporter genes are presently ongoing and identification of these genes will significantly improve our understanding of drug and nutrient transporters of kinetoplast parasites.

Notes:

4. Site-directed mutagenesis of specific amino acid residues supports the model of conductance of pentamidine through the TbAQP2 channel

Authors: Ali E Alghamdi1, 2, Jane C. Munday1, and Harry P. de Koning1
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Abstract:

African trypanosomes cause sleeping sickness in humans, a disease that is typically fatal without chemotherapy. The treatment of HAT is based on just a few drugs: Eflornithine, Pentamidine, Melarsoprol, Nifurtimox and Suramin. The extensive use of the available drugs led to the emergence of drug resistance. Unfortunately, resistance to some of the drugs has reached alarming levels and appears to be spreading, but our comprehension of the resistance mechanisms remains incomplete. Aquaporins (AQPs) are integral membrane proteins functioning as the cellular entry pathways for antimony oxides in *Leishmania* species, and in general are the conduit for glycerol, small sugars, inorganic arsenic and water. In virtually all organisms the regulation of osmotic pressure is an important role of aquaporins. The aquaporins are of different sub-types: in human tissues there are about 13 of aquaporins, and hundreds have been identified in a multitude of non-human species. In *Trypanosoma*, three aquaporins genes, AQP1-3, have been identified. Recent studies have revealed that there is a genetic link between this gene and drug susceptibility, leading to the hypothesis that some of the clinical trypanocides, specifically pentamidine and the melaminophenyl arsenicals enter through these aquaporins. In *T. brucei* aquaporins 2 and 3 genes are found on chromosome 10 in a tandem array and share 83% sequence identity. Specifically, TbAQP2 was found to be a highly efficient transporter for pentamidine and melarsoprol and introduction of this gene into *Leishmania mexicana* made these parasites more than 1000-fold more sensitive to melarsoprol, and 40-fold more sensitive to pentamidine. Therefore, an understanding of the mechanisms of AQP2-mediated drug uptake in African trypanosomes will facilitate the advancement of diagnostic tools and perhaps at the same time the improvement of enhanced treatments. We report here the construction of several genetic mutations (single or multiple amino acid substitutions) in AQP2 to investigate their effects on the ability of the gene for drug sensitivity and drug transport. As part of this strategy, leucine residues were replaced by tryptophan in three suggested sites in the Tb AQP2 gene. The results of introducing tryptophan residues in L84 and L118 in the TbAQP2 showed some loss of pentamidine susceptibility compared to the wild-type cells, whereas L218 showed equal sensitivity to pentamidine compared to the wild-type cells. A double mutant of L84W/L118W displayed an even greater loss of pentamidine susceptibility.

Notes:

5. Essentiality of pSCL4, a Giant Linear Plasmid of Streptomyces clavuligerus.

Authors: Lis Algora, Paul R. Herron
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Abstract:

Clavulanic acid is a β-lactamase inhibitor that is used in combination with the β-lactam antibiotic Amoxicillin. It is produced by *Streptomyces clavuligerus* (phylum *Actinobacteria*) whose genome includes a linear chromosome and four linear plasmids pSCL1, pSCL2, pSCL3 and pSCL4. With a length of 1.8 Mb, pSCL4 is the largest linear plasmid sequenced to date. It carries 20% of the *S. clavuligerus* coding sequences, none of which are thought to be involved in the primary metabolism of the bacterium and therefore its essentiality is questionable. However, sequencing results showed that the genes encoding the terminal proteins Tap and Tpg were located on pSCL4. These proteins are necessary for telomere replication of linear replicons in streptomycetes. As *tap* and *tpg* are absent from the chromosome, it suggests that *S. clavuligerus* might rely on these plasmid-encoded proteins to maintain the chromosome ends. In this study we have confirmed that *tap* and *tpg* are present as single copies in the genome of *S. clavuligerus* type strains which indicates the essential role of pSCL4. Further experiments involving deletion of the *tap-tpg* operon from pSCL4 will confirm their role on maintenance of chromosomal linearity and telomeric sequences. Moreover, we have constructed *S. clavuligerus* mutants complemented with second copies of *tap-tpg* that we predict leave pSCL4 dispensable for growth of the bacterium.

Notes:

6. Multidrug Resistant Acinetobacter baumannii: An Emerging Health Threat in Aseer Region, Kingdom of Saudi Arabia

Authors: Mohammed K. Almaghrabi1,*, Martin R.P. Joseph1, Mohammed M. Assiry2, Mohamed E. Hamid1
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Abstract:

The study aims to determine the prevalence of multi-drug resistant *A. baumannii* in Aseer region, Kingdom of Saudi Arabia. **Methods**: This study evaluated the antibiotic susceptibility of ninety four (n =94) clinical isolates of *A. baumannii*. The isolates were collected from the south region of Saudi Arabia; and notably Aseer region, during the period from 15 October 2014 to 15 January 2015. The isolates were tentatively identified as *A. baumannii* by routine bench tests; and were confirmed by using VITEK® 2 Compact. The latest instrument was used to identify antibiotic susceptibility of these isolates. **Results:** Antibiotic susceptibility in this study showed that 69% of these isolates were multi-drug resistant strains. Moreover, they were highly resistant to carbapenem drugs. Several strains of these isolates were found to be extremely resistant to test antibiotics, and were only sensitive to one or two of them. **Conclusion:** High rate of multi-drug resistance A. *baumannii* bacteraemia has emerged in the south region of Saudi Arabia as an important health problem. Therefore, it is considered as a new threat in hospitals, which requires a tremendous effort to stop its escalation and spread.

Keywords: Acinetobacter *baumannii*, Antibiotic, Bacteraemia, Carbapenem, Susceptibility

Notes:

7. Developing protein antibiotics for treatment of AMR *Pseudomonas aeruginosa*

Authors: Madhuri Barge, Anne Six, Daniel Walker
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Abstract:

Antibiotic resistance is a global health threat and without discovery of new antibiotics we are heading towards a pre-antibiotics era where bacterial infections will become deadly. In our lab we work on a group of protein antibiotics produced by gram negative bacteria that have evolved to win and survive the intra species competition. One such protein antibiotics is pyocin S5 produced by *Pseudomonas aeruginosa*. We intend to develop a pyocin S5 as a highly specific therapeutic for the treatment of *Pseudomonas aeruginosa*, the major cause of death in patients suffering from cystic fibrosis (CF). The primary objective is to generate methods for the production, formulation, manufacture and delivery of pyocin S5 and a safety profile for delivery by inhalation. To achieve this we have developed a method for pyocin S5 purification. We have tested the lyophilised protein at various time interval and temperatures to evaluate suitable formulation conditions. The long term and short-term stability tests were carried out for the formulated protein. Pyocin S5 has a great potential for development as a much needed therapeutic drug to treat antibiotic resistant Pseudomonas aeruginosa infection and might be a suitable drug for treating people with cystic fibrosis.

Notes:

8. Novel Antimicrobial Mechanisms in Phagocytic Cells

Authors: Massimiliano Baldassarre, Domenico Mancuso and Stefania Spanò.
Affiliation: *Institute of Medical Sciences, University of Aberdeen, Aberdeen UK*
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Abstract:

Enhancement of host defences represents a possible strategy for combating infections and reduce antimicrobial resistance. Mechanisms underpinning bacterial clearance and the strategies used by pathogens to avoid it are not completely understood.

We previously identified a host trafficking pathway that prevents the human-restricted bacterial pathogen *Salmonella* Typhi from surviving in mouse macrophages. This antimicrobial pathway depends on the host GTPase Rab32 and its guanine nucleotide exchange factor BLOC3. We showed that in contrast to *Salmonella* Typhi, the broad-host pathogen *Salmonella* Typhimurium infect mice by counteracting the Rab32 trafficking pathway through the delivery of two type-III-secretion effectors: 1) GtgE, a specific protease cleaving Rab32; and 2) SopD2, a Rab GTPase activating protein. By neutralising this host defence pathway, GtgE and SopD2 allow *Salmonella* Typhimurium to establish a systemic infection.

Our recent results indicate that *Salmonella* is not the only pathogen susceptible to the BLOC3/Rab32 antimicrobial pathway and suggest that other intracellular pathogens have evolved to neutralise this host-defence pathway to be able to survive phagocytic cells and to cause infection. Mechanisms underlying these antimicrobial processes and bacterial counteractions are currently being investigated. Boosting of this antimicrobial pathway could be exploited in the future to prevent or treat bacterial infections.

Notes:

9. Development Of Streptomyces To Utilise Sustainable Feedstock In Fermentations

Authors: Anna S. Birke1, Steve G Kendrew, Paul R Herron, Ben Huckle, Iain S. Hunter1 & Paul A. Hoskisson*1
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Abstract:

Members of the *Streptomyces* genus have been used in industry for decades to produce bioactive specialised metabolites, such as antibiotics. Primary metabolic intermediates are required for the biosynthesis of these compounds. In fermentations, the carbon source available during the production phase has been shown to have a profound impact on antibiotic production via carbon source-dependent regulatory mechanisms, such as carbon catabolite repression. Since bacteria usually exhibit preferences of one carbon source over another with the former often being glucose, the range of carbon sources that can be utilised in fermentation media is often key to the fermentation performance. We are interested in broadening and optimising the catabolic capabilities of selected *Streptomyces* strains, including the indrustrially relevant *S. clavuligerus* and the model organism *S. coelicolor*, to allow usage of carbon sources obtained from sustainable feedstocks. Using a combination of bioinformatics and molecular genetics we are comparing actinobacterial carbon uptake and catabolic systems, as well as constructing integrating vectors for the heterologous expression of either a sugar permease or sugar kinase from *Streptomyces* species. The genes are placed under the control of an inducible promotor to enhance their expression in the cells and allow characterisation of growth and antibiotic production phenotypes.

Notes:

10. Using individual-based mathematical models to study antibiotic resistance

Authors: Dr Ruth Bowness, Professor Mark Chaplain, Dr Gibin Powathil, Professor Stephen Gillespie
Affiliation: University of St Andrews, University of Swansea
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Abstract:

I have developed a novel individual-based mathematical model to study pulmonary tuberculosis (TB) disease progression, the response to treatment and the risk of resistance. Using discrete elements that mimic the spatio-temporal interactions of bacteria and T cells, the movement of cells is governed by biased random walks, whilst interactions are governed by rules defined by other published data. Diffusion of chemokines, oxygen and antibiotics are modelled through partial differential equations. This model is capable of simulating multiple antibiotics via an integrated pharmakokinectic/pharmcodynamic model. This model is currently being extended to investigate new treatment approaches for multi-drug resistant (MDR) and extensively-drug resistant (XDR) TB. Early results show that spatial differences in antibiotic diffusion make it more likely that resistance will develop. Such individual-based models have considerable potential to address this complex question. It is simple to adapt the framework to address other important antibiotic resistant infections and our next target is the study of carbapenem-resistant Enterobacteriaceae (CRE) in urinary tract infections (UTIs).

Notes:

11. Detection of AMR and co-selectors in drinking water

Authors: Dr Helen Bridle
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Abstract:

A NERC funded collaboration with India has just started focussing on the detection of AMR and co-selectors in drinking water. The aim is to develop new sensor technologies to support case studies of AMR in Indian waters utilising the data to model AMR and co-selector interactions and benchmark sensor performance against existing techniques. The project will run from 2018-2021 and this poster will give an overview of the project plans and aims. Several workshops and meetings will be held both in Scotland and India and we would be interested to discuss with potential stakeholders or other academics to expand the reach of the project.

Notes:

12. Understanding the chemical warfare of actinomycetes across taxonomic and phylogenetic boundaries for accelerated antibiotic discovery

Authors: Laia Castano Espriu and Katherine Duncan, University of Strathclyde
Affiliation: Paulina Rakowska, National Centre of Excellence in Mass Spectrometry Imaging, National Physical Laboratory, Teddington
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Abstract:

The bacterial order actinomycetes, is the major producer of specialized metabolites with diverse biological activities. Approximately 45% of all antibiotics in clinical use today are produced by actinomycetes. Depending on their genome size, actinomycetes may contain over 30 biosynthetic gene clusters encoding for specialised metabolites. However, only a small fraction are transcribed under normal laboratory coniditions. It has been observed that interspecies interactions may play a role in the induction of specialized metabolites. There is a vast number and taxonimc diversity of bacterial strains which might compete with actinomycetes to maintain an ecological advantage. Metabolites are likely produced as a defence mechanism. Therefore, a co-culture technique is an effective method to achieve interactions between bacteria.

To understand the chemical exchange between strains across taxonomic and phylogenetic boundaries, the impact of microbial interactions was assessed on the strains ability to produce specialised metabolites. To investigate this topic, liquid co-culture technique was used for metabolites extraction. Furthermore, the bioactivity of all metabolite extracts were tested against ESKAPE pathogens. Liquid chromatography tandem mass spectrometry (LC-MS) was perfomed to obtain the metabolite profiles. GNPS molecular networking has enabled the dereplication of biological extracts and comparison across the different experimental conditions. Chemically interesting interactions will be subjected to Imaging Mass Spectrometry (IMS) in collaboration with the National Phyiscal Laboratory. The results demonstrate that microbial interactions in actinomycete strains isolated from marine environments together with the recent advances in mass spectrometry and comparative metabolomics represent an exicitng strategy for prioritizing novel chemistry to combat antimicrobial resistance.

Notes:

13. Longitude Prize

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Abstract:

Three hundred years after the original Longitude prize, the British public was asked to consider 6 globally relevant issues and to vote on the one they deemed to be of most immediate public importance. The winning challenge was how to reduce the use of antibiotics.
The Longitude Prize 2014 is a £10m prize fund that will reward a competitor that can develop a point–of–care diagnostic test that will conserve antibiotics for future generations and revolutionise the delivery of global healthcare. The test must be accurate, rapid, affordable and easy to use anywhere in the world.
Point-of-care test kits will allow more targeted use of antibiotics, and an overall reduction in misdiagnosis and prescription. Effective and accurate point of care tests will form a vital part of the toolkit for stewardship of antibiotics in the future. This will ensure that the antibiotics we have now will be effective for longer and we can continue to control infections during routine and major procedures.
This poster will look to inform you further about the problem of antibiotic misuse and how the Longitude prize hopes to help tackle this.

Notes:

14. Role of Implant Nanoroughness and Bioactive coating on Osseointegration and Bacterial Growth

Authors: Laila Damiati1, Virginia Llopis-Hernández1, Mark Ginty2, Angela Nobbs2, Bo Su2, Gordon Ramage3, Richard Oreffo4, Penelope M. Tsimbouri1, Manuel Salmeron-Sanchez1, Matthew J. Dalby1
Affiliation: [1]*Centre for Cellular Microenvironment, University of Glasgow, Glasgow, UK;*
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Abstract:

We are investigating the osseointegration and antimicrobial properties against *Pseudomonas aeruginosa* of Titanium nanotopographies. Poly(ethylacrylate) (PEA) causes a spontaneous unravelling of fibronectin upon contact which facilitates interaction with growth factors (GF), allowing ultra-low dose GF presentation with high efficiency. We are thus studying the effect of Ti bactericidal nanotopographies coated with PEA/FN/BMP2 to see if the coating can improve MSC growth and differentiation while maintaining bacterial kill.
Ti nanowire surfaces produced through a thermal oxidation under alkaline conditions. Surfaces were coated with PEA using a plasma polymerisation. The biological coating was applied using FN/BMP2 prior to Stro-1^+ hBM-MSC culture. Physical and chemical characteristics were studied using SEM, AFM, WCA, and XPS.

Polymer coating increased the hydrophobicity of Ti, which increased protein adsorption. FN decreased the hydrophobicity, which improved cell adhesion. The number of cell-binding domains as well as the heparin-binding domain increased on the coated surfaces compared to coated/ uncoated flat surfaces. The current coating showed an improvement of cell growth, adhesion and osteogenic gene expression on TiO_2 nanowire surfaces.
An ideal bone implant should improve the osteogenesis and reduce bacterial adhesion. However, increasing the implant surface area, e.g. a 3D format could improve the osteogenic and bactericidal effect we seek.

Notes:

15. Novel Streptomyces compound discovery by LC/MS guided screening of growth conditions

Authors: Joshua Burns[1,2], Christine Edwards[1], Linda Lawton[1] & Samantha Law[2]
Affiliation: [1]The Robert Gordon University, School of Pharmacy and Life Sciences, Aberdeen AB10 7GJ
[2]NCIMB Ltd, Craibstone Estate, Aberdeen AB21 9YA
E-mail: c.edwards@rgu.ac.uk

Abstract:

Streptomyces species are a major source of antibiotics but are often grown under restrictive conditions that limit biosynthetic gene expression. The overarching aim of this study was to identify conditions that produce novel antibiotics, specifically against Gram-negative pathogens.
Rare *Streptomyces* from the Culture Collection NCIMB were inoculated into 24-well plate screens, with each plate containing 8 conditions. Nutritional screening used different carbon and nitrogen sources, with agar and broth equivalents. Stresses and elicitors included solvents, metals, and antibiotics. Samples were taken at 5, 10 and 15 days for UPLC/MS analysis, and the resulting Data processed with MZmine. *S. sp.* was selected for scale-up as it had shown bioactivity against *Escherichia coli* with > 90% inhibition using the XTT assay. Genome mining also identified over 20 biosynthetic gene clusters with less than 50% homology to known biosynthetic gene clusters.. Principal Component Analysis showed clear separation between solid, liquid, and time points. In medium M19, 39% of metabolites were found only in liquid media, and 19% in solid. *S. sp.* was grown in liquid M19 for 5 days. The supernatant was run through a C18 column, and flow through loaded into a high polarity retention resin. High polarity fractions are less studied so may contain novel metabolites.

Initial dereplication identified common compounds such as Actinomycins C, D, and Desferrioxamine. MS/MS spectra were obtained for these compounds and the remaining unidentified metabolites. Novel metabolite discovery in *Streptomyces* can be enhanced through a combination of genomic and metabolomic tools.

Antimicrobial resistance is predicted to cause 10 million a year, with a cumulative cost of $100 trillion by 2050 (1). Increasing the chemical space from *Streptomyces* is a valuable method to contribute to the drug development pipline.

1: Tackling drug-resistant infections globally: final report and recommendations: The review on Antimicrobial Resistance

Notes:

16. Mutants versus cations: variable effects on biofilm formation by Pseudomonas aeruginosa PA14

Authors: Alistair Grant and Georgios Efthimiou
Affiliation: University of Strathclyde
E-mail: georgios.efthimiou@strath.ac.uk

Abstract:

Pseudomonas aeruginosa is an on-going health hazard for hospitals and water systems, as formation of biofilms makes its eradication rather difficult. In this study, the effect of inorganic salts (10 mM final concentration) on biofilm formation by P. aeruginosa PA14 on plastic surfaces was examined, daily up to 96 h. The addition of lithium, manganese and calcium ions significantly speeded up biofilm formation by PA14. Furthermore, knockout mutants of five biofilm-related PA14 genes were then tested as above, namely cupB5, PA3357, vfr, rh1A and ampR. For the PA3357, vfr, rh1A and crc mutants, the formation of biofilms without the addition of salts was lower than the wild type. A substantial increase in biofilm formation in ampR was observed. Biofilm formation by the vfr mutant was significantly increased by addition of calcium ions. Lithium ions had the same effect for the rh1A mutant, while biofilm formation by the PA3357 mutant was enhanced by addition of lithium, magnesium, manganese and calcium ions. Conversely, the addition of any cation in the ampR knockout appears to inhibit biofilm formation. Our results suggest that biofilm formation by *P. aeruginosa* PA14 is selectively regulated by specific cations rather than simply by changes in surface charge.

Notes:

17. Evaluation of greater wax moth larvae, Galleria mellonella, as a novel in vivo model for non-tuberculosis Mycobacteria infections and antibiotic treatments

Authors: Frances Entwistle
Affiliation: University of St Andrews
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Abstract:

Galleria mellonella, the larvae of the greater wax moth, are an increasingly popular whole-organism model for a variety of infectious microorganisms, and are a valuable tool for performing rapid, cost-effective screens of existing and novel treatments for these infections. Here, we present our use of *Galleria* larvae as an *in vivo* model and drug-screening tool for mycobacteria infections. The bacteria utilised were *M. fortuitum, M. marinum* and *M. aurum* -– larval survival decreased after infection with *M. fortuitum* and *M. marinum* in a dose-dependent manner, but remained unaffected by *M. aurum*. Heat-killed bacteria did not cause larval death. Where antibiotic monotherapy was efficacious, larval survival post-infection increased in a dose-dependent fashion. However, efficacy varied between different antibiotics and species of infecting mycobacteria. Combinations of antibiotics led to higher survival of infected larvae than antibiotic monotherapy. Selected antibiotic treatments that enhanced larval survival reduced the overall internal burden of infecting mycobacteria, but did not eradicate the pathogens. Administration of amikacin or ethambutol to uninfected larvae induced an initial transient increase in the numbers of circulating haemocytes and reduced the phagocytic rate of haemocytes in larvae infected with *M. marinum*.

Notes:

18. Assessing the impact of changes in national antibiotic use in Scotland on Gram-negative resistance using the NHS Scotland Infection Intelligence Platform

Authors: William Malcolm, Charis Marwick, Jenny Armstrong, Kim Kavanagh, Guy McGivern, Marion Bennie
Affiliation: National Health Scotland
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Abstract:

Background
Since 2008 use of broad-spectrum antibiotics associated with increased risk *of Clostridium difficile* infection (CDI) has reduced across Scotland. This study investigated associations between use of these antibiotics and antimicrobial resistance (AMR) among Gram negative bacteraemia.

Methods
Antibiotic use data (2009-14) were extracted from Hospital Medicines Utilisation Database and Prescribing Information System and combined defined daily doses (DDD) per 1000-population-per-month calculated for co-amoxiclav, fluoroquinolones and 3rd-generation cephalosporins. Data on *E.coli* and *Klebsiella* bacteraemias were extracted from routine national data. Binomial general linear regression was used to quantify associations between proportion resistant bacteraemias and antibiotic use.

Results
Use of fluoroquinolones and co-amoxiclav was 35% lower, and cephalosporins 41% lower, in 2014 compared to 2009, with significant trends over time. Resistance to cephalosporins and fluoroquinolones decreased among *E.coli* (relative reductions of 24% and 17% respectively). There were no changes in *Klebsiella* resistance. There were significant associations between antibiotic use and *E.coli* resistance for cephalosporins OR1.07 (95% CI 1.02–1.13); interpreted as 7% (2-13%) increase in resistance with each additional DDD/1000-population, fluoroquinolones [OR1.02 (1.01–1.03)] and co-amoxiclav [OR1.01 (1.01–1.01)].

Conclusions
Reductions in use of antibiotics with high CDI risk has been associated with reduced resistance among *E.coli* but not *Klebsiella* bacteraemia.

Notes:

19. Characterisation of risk factors associated with antibiotic resistance in urinary isolates in the community: an exemplar of NHS Scotland's Infection Intelligence Platform

Authors: William Malcolm, Eilidh Fletcher, Kim Kavanagh, Camilla Wiuff, Ashutosh Deshpande, Charis Marwick, Marion Bennie
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Abstract:

Background
The threat from resistance to multiple antibiotics is growing. Multidrug resistance reduces treatment options and increases the potential for treatment failure. In the community urinary tract infections (UTI) are common and antibiotic treatment usually empirical. This study used routine national data to characterise factors associated with antibiotic resistance in urine isolates.

Method
Urine isolates from national surveillance (2012 to 2015) were linked with hospital activity and community prescribing datasets at patient level. Risk factors associated with resistant and multi-resistant isolates were assessed using multivariable multinomial logistic regression.

Results
Of 40,984 isolates: 45% were resistant; 27% multi-resistant; and 28% susceptible to the antibiotics tested. Antibiotic exposure in the 6 months prior to a urine isolate was strongly associated with multi-resistance; those prescribed ≥ 4 different antibiotics had OR6.09 (95% CI 5.16-7.19). Cumulative antibiotic exposure had a dose-response relationship - multi-resistance was observed in individuals with $\geq$29 DDD of any antibiotic (OR6.54; 95% CI 5.88-7.27) in the 6 months prior to the isolate.

Conclusion
This study identified, and quantified, risk factors for multi-drug resistance in urine isolates. This evidence base is now informing development of patient-centred prescribing decision support tools for treatment of UTI and to improve antimicrobial stewardship.

Notes:

20. Whole Genome Sequencing (WGS) of Enhanced Surveillance Escherichia coli and Staphylococcus aureus Bacteraemias (ECB and SAB) to investigate the development of AMR in Scottish National Health Service (NHS) health boards

Authors: Dr. Stephen Fox 1, Dr. Cosmika Goswami 1, Dr. Kerry Pettigrew 2, Dr. Robin Young 3, Dr. Elizabeth Dickson 4, Laura Imrie 5, Dr. Fiona Murdoch 5, Dr. Martin Connor 6, Prof. John Coia 4, Prof. Colin McCowan 3, Prof. Matthew Holden 2, Prof. Alistair Leanord 1, Prof. Thomas Evans 1
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5 Health Protection Scotland, Clifton House, Clifton Place, Glasgow, UK
6 Department of Microbiology, Dumfries and Galloway Royal Infirmary, Dumfries, Scotland, UK
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Abstract:

Escherichia coli and *Staphylococcus aureus* are the two main infective organisms that cause bacteraemia. Bacteraemias are a significant and growing cause of patient mortality and morbidity. This growth in bacteraemias is considered to be due to an increase in AMR. To investigate AMR development we collected ~700 ECB and SAB isolates with Enhanced Surveillance data from NHS health boards across Scotland (2013-2015) for whole genome sequencing.

We identified the key AMR genes in both ECB and SAB isolates. The ECB strain ST131 and the SAB strain ST22 both had significantly higher AMR genes and both predominated in hospital-associated infections (HAI).

Network analysis of AMR genes and phenotypic resistances showed strong associations between antibiotics that are largely confined to hospital use *e.g.* 3rd generation cephalosporins). This suggests, current antibiotic use is generating cross-resistance to other AMR agents, probably through the acquisition of plasmids containing multiple AMR determinants.

Genome-wide association studies (GWAS) and Random Forest classification of AMR SAB genes was performed in linkage with clinical data. The *qac* AMR genes were highly associated with HAIs and in patients with eczema or other skin break risk factors.

Whole genome sequencing with enhanced surveillance data may identify the key AMR determinants that regulate the complex host/microbial interactions.

Notes:

21. How does Staphylococcus aureus adapt, survive and cause infection? A molecular approach for the identification of novel antibiotic targets.

Authors: Andreas F. Haag
Affiliation: Institute of Infection, Immunity and Inflammation, University of Glasgow, G12 8TA Glasgow
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Abstract:

S. aureus can cause a huge variety of diseases as it is able to adapt its lifestyle to many distinct microenvironments found in the diverse host niches it inhabits. To adapt to changing host environments, *S. aureus* needs to sense changes in its surrounding and alter its metabolism in a way that best ensures its survival. To this end, *S. aureus* contains 16 individual signalling relays called two-component signal transduction systems (TCS). These molecular sensors can be considered as the eyes and ears of the pathogen and trigger adaptive changes in the bacterium following the exposure to a signal. Apart from very few cases, the signalling molecules sensed by these TCS are mostly unknown and the precise networks of genes specifically targeted by them are not well defined.

Adaptation to changing environments is crucial for staphylococcal survival during infection and therefore presents an attractive target for developing new drug/antibiotics that can prevent *S. aureus* to respond to external stimuli. We aim to define the signalling cascade of *S. aureus* TCS and their role in bacterial adaptation and virulence. This research will eventually provide us with new targets for the treatment and prevention of *S. aureus* infections.

Notes:

22. Genomic Mining of Thermophilic Actinobacteria for Novel Antibiotics

Authors: Gillian Halket, Katherine Duncan and Paul Herron
Affiliation: Strathclyde Institute of Pharmacy and Biomedical Sciences, University of Strathclyde, Glasgow
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Abstract:

The overuse of antibiotics has led to microbial infections continually evolving resistance, creating an acute need to discover new drugs. This research project aims to revisit natural antibiotic discovery in this post-genomic era, by applying genomic mining techniques and for the first time, combining it with recently developed methods of molecular networking.

Over 50% of antibiotics are produced by mesophilic Actinobacteria, yet thermophilic Actinobacteria have also historically yielded important compounds such as the antibiotics thermomycin and anthramycin. Most compounds from mesophilic Actinobacteria are thermolabile resulting in the potential loss of effectiveness during storage. Consequently, revisiting extreme environments with a view to exploration of thermostable alternatives to currently available antibiotics, may provide bioactive compounds with enhanced properties.

Seventeen putative thermophilic Actinobacteria have been isolated from compost. Their physical attributes were recorded and their identity is being determined by 16S rRNA sequencing. The ability of each strain to kill a panel of ESKAPE pathogens will then be analysed, indicating potential bioactive compounds. Next generation DNA sequencing will be applied to candidate strains and potential gene clusters encoding bioactive compounds predicted. Metabolite profiling linked to temperature based de-replication will be used, followed by a molecular networks approach in combination with the genomic data, identifying metabolites that are known antibiotics and those that are truly novel.

Notes:

23. Rapid phenotypic susceptibility testing of bacteria: SLIC by name and slick by nature

Authors: Robert J. H. Hammond, Kerry J Falconer, Tom H Powell, Stephen H. Gillespie
Affiliation: University of St Andrews
E-mail: rjhh@st-andrews.ac.uk

Abstract:

Tools to detect the susceptibility of bacteria rapidly are necessary if we are to turn the tide of increasing antimicrobial resistance. Until a comprehensive set of molecular diagnostic tools are produced phenotypic resistance will remain necessary.

We have integrated several technologies in our novel susceptibility methodology. SLIC: Scattered Light Integrated Collector which is a method of detecting very small numbers of bacteria, approximately 10/mL. We harness this to determine susceptibility rapidly. We present data that shows that we can distinguish phenotypic susceptibility from resistance in minutes. This means that a result is available in a much shorter time than conventional methodologies: E. coli, S. aureus, and K. pneumoniae results are all available in less than 3, 5 and 10 minutes, respectively. The testing platform is robust and could be automated it is, moreover, easy to produce at high volume and low cost.

SLIC susceptibility compares favourably with the published turn-around time for other devices on the market. VITEK2 (standard of care in Scotland) takes >7 hours to determine MIC breakpoints for pathogens whereas it takes SLIC <30 minutes for multiple antibiotics.

Detecting susceptibility rapidly is essential. A tool such as SLIC-susceptibility could be the ideal partner for MALDI-TOF identification allowing a comprehensive organism characterisation within an hour of isolation. Such a development could transform the diagnostic landscape.

Notes:

24. Investigations into terpenoids action on the Shigella sonnei protein, DsbA by enzymatic kinetic assay

Authors: Thaer Hasan[a,b], Veronique Seidel[a] and Paul Herron[a]
Affiliation: [a]Strathclyde Institute of Pharmaceutical and Biomedical Sciences, University of Strathclyde, Glasgow, UK, G4 0RE,
[b] University of Anbar, Ramadi, Anbar, Iraq
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Abstract:

Multidrug resistant (MDR) *Shigella* strains have now become prevalent worldwide especially in developing and newly-industrialised countries. DsbA is a bacterial periplasmic thiol-disulphide oxidoreductase and is the key component of the disulphide bond family enzymes. DsbA catalysis the folding of secreted proteins of which many are virulence factors. Terpenoids are one of novel agents which used as anti-virulence by targeting the activity of DsbA. The first labelling of Di-E-GSSG was successful and the product showed an increasing in RFU after adding reducing factor (DTT). DsbA protein is showed ability to convert Di-E-GSSG into E-GSH within 15 min. Geraniol is one of twelve terpenes that used in this study showed a significant activity in inhibition of reducing state by DsbA. *In vivo* experiments, *S. sonnei* wild type and complementary one can catalysis the E-GSH and form Di-E-GSSG again when compared to DsbA mutant strain. Geraniol can also inhibit this catalyst when it was added to media with same 42µM concentration. To our knowledge, this is the first time that *Shigella* DsbA has been shown to catalase GSH to GSSG, which strongly support the hypothesis that catalysis of GSH to GSSG in the host cell cytosol is imperative for *Shigella* to survive, proliferate and establish infection. Geraniol is consider a novel agent and promising anti-virulence therapeutic in *Shigella* infection by targeting DsbA protein.

Notes:

25. Antimicrobial resistance (AMR): which measures should we use?

Authors: R. W. Humphry, S. C. Tongue, J. Evans, C. Webster, G.J. Gunn
Affiliation: SRUC, Scotland's Rural College
E-mail: Roger.Humphry@sruc.ac.uk

Abstract:

It is not clear that when we measure antimicrobial resistance we always use the best measure. Surveillance should be appropriate for the questions in hand. Existing global AMR surveillance has various limitations and of greatest importance to this study are: a) studies are frequently based on clinical samples (bias); b) there is a lack of evidence-based standardization. Typically the method chosen involves the selection of a single isolate per sample and testing of that isolate. In this poster we describe the results for one antibiotic against *E. coli* and demonstrate that the **perceived** level of resistance is greatly dependent on the method chosen. Direct plating method was much more likely (34%) to show resistance than testing seven individual isolates (15%). This evidence is a reminder that prevalence estimates are very sensitive to the method of measurement used and, therefore, that the method should be appropriate for the question being addressed.

Notes:

26. Synthetic Phage-inducible Chromosomal Islands, the Trojan Horse against AMR.

Authors: Rodrigo Ibarra-Chavez1,2, Jonathan M. Cooper1, Jose R. Penadés2
Affiliation: [1]Division of Biomedical Engineering, College of Science and Engineering, University of Glasgow, Glasgow, UK
[2]Institute of Infection, Immunity and Inflammation, College of Medical, Veterinary and Life Sciences, University of Glasgow, Glasgow, UK
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Abstract:

With the emerging global threat of antimicrobial resistance (AMR), diagnosis and treatment of infectious diseases has become more difficult than ever. We need to consider new paradigms in therapy and innovative alternatives that can allow us to rapidly detect bacteria at the point-of-care. Here we use synthetic phage-inducible chromosomal islands (PICIs) to combine the two concepts of diagnostics and therapy to "seek & destroy" specific bacteria. These novel biosensors allow the detection and elimination of the pathogen by using the pathogen itself to modify its genome specifically to produce a reporter (seek) and/or a killing switch (destroy).

Detection of pathogenic bacteria is achieved by targeted transfer of a fluorescent reporter gene, which can easily be visualised. We have also adapted the detection protocol for the use in low-cost, portable paper microfluidic devices. Elimination of the pathogen is facilitated by the delivery of a CRISPER-Cas9 system targeting methicillin resistance in *Staphylococcus aureus* or other antibiotic resistance cassettes in *Escherichia coli*. Thus, PICIs provide a versatile platform for the detection and targeted elimination of specific bacterial pathogens.

Notes:

27. Cephalosporin resistance levels can be significantly influenced in members of a novel E. coli multidrug-resistant, ESBL-producing clade.

Authors: Marta J Piotrowska1, Susan Harris1, Robert J Goldstone1,2, Ruby Qi1, David GE Smith1
Affiliation: [1]Heriot-Watt University, IB3, Edinburgh, EH14 4AS
[2]The Francis Crick Institute, London, NW1 1AT
E-mail: m.piotrowska@hw.ac.uk

Abstract:

The problem of antimicrobial resistance (AMR) is an increasing concern in the present world and multidrug resistance (MDR) to several classes of antibiotics is becoming one of the major public health threats. *E. coli* is one of the WHO "high priority" organisms in which antibiotic resistance is widespread. In *E. coli* AMR is encoded in core and accessory genome and we carried out a genomic survey of antibiotic resistance on the population level to determine the distribution of resistance genes across *E. coli* phylogenetic groups. Some *E. coli* subgroups show particularly high prevalence of MDR. Cephalosporins represent one of the frontline antibiotic groups used to treat *E. coli* infections. Cephalosporins belong to the wider class of β-lactam antibiotics and many are "essential medicines". Later (3^{rd} & 4^{th}) generation cephalosporins are susceptible to Extended Spectrum β-lactamase (ESBL)-producing strains and are highlighted as a particular concern. We are investigating responses of ESBL-producing *E. coli* to cephalosporins through exploration of the resistance profiles to different cephalosporins and how environment (oxygen and pH) shape the response of ESBL strains to these antibiotics.

Notes:

28. Micro technologies for fast bacteria separation and purification from clinical samples

Authors: Melanie Jimenez, Julien Reboud and Jon Cooper
Affiliation: Biomedical Engineering Division, University of Glasgow
E-mail: Melanie.Jimenez@glasgow.ac.uk

Abstract:

Traditional methods to identify an infection are based on bacteria culture and require several days to establish a positive result. During this interim period, potentially ineffective broad-spectrum antibiotics are often administered that may lead to the emergence of resistant bacteria. Our work tackles the challenge of rapid diagnosis by engineering a suite of new microsystems capable of performing fast, user-friendly purification of bacteria from clinical samples. Recognised as a key enabling step within the diagnostic workflows (before detection), sample processing remains a challenge due to i) the low concentration of bacteria in bodily fluids, ii) the difficulty in processing often complex fluids (*e.g.* blood) and iii) the wide range of bacteria species to be detected. Here, we combine new microfluidic-based separation approaches with smart bio-mimicking receptors to isolate, within minutes, harmful bacteria in small volumes of fluids (<100ml). These technologies will promote the use of currently limited, advanced bacteria detection and characterisation assays, e.g. using next generation sequencing, which require fast sample processing for diagnostics close to the patient at the point of need. The technologies proposed here have the potential to fasten adoption of such advanced approaches in the clinical workflow, enabling a targeted and personalised approach to therapy.

Notes:

29. The Use of Differentiated Airway Epithelial Cell Cultures for Assessing Antibiotic Transport and Activity within the Bovine Respiratory Tract

Authors: Claire Jones, Catherine Berry, Robert Davies
Affiliation: University of Glasgow
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Abstract:

Mannheimia haemolytica is considered one of the most prevalent bacterial agents associated with bovine respiratory disease (BRD). The emergence of antibiotic-resistant strains of this pathogen represents a serious threat to the control of BRD and the development of new therapeutics are urgently required. However, there is currently a lack of appropriate *in-vitro* models for studying drug transport and efficacy in the veterinary field. This study utilized differentiated bovine airway epithelial cells (BAECs) grown at air-liquid interface to assess transport and antimicrobial activity of selected antibiotics used in BRD treatment. We first investigated the transport of five antibiotics across the epithelium and demonstrated differing rates of transport. These results suggest differences in the transport properties of the antibiotics and/or the presence of different transport mechanisms. Using a metaphylactic treatment approach, we next demonstrated that marbofloxacin provided immediate antimicrobial activity and prevented infection of epithelial cells with *M. haemolytica*. Using a therapeutic treatment approach, we subsequently showed that marbofloxacin and florfenicol exhibited delayed antimicrobial activity although the bacteria were eventually eliminated and tissue recovery followed. This study has highlighted that differentiated BAECs can be used to study antibiotic transport and activity and offers a potential *in-vitro* screening tool for drug development.

Notes:

30. Characterization of virulence factors in Leishmania mexicana by comparative Omics approaches

Authors: Abdulbaset Kabli, Michael Barrett, Richard Burchmore
Affiliation: University of Glasgow
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Abstract:

Leishmania have the ability to hijack the host immune system and adopt sophisticated strategies, involving virulence factors, to develop and survive within the mammalian host. Leishmania parasites survive within macrophages, inside a parasitophorous vacuole, by modulating macrophage signaling pathways. The molecular communication between host and parasite decides the outcome of infection, but is incompletely understood. We have compared genotype and phenotype of an attenuated *Leishmania mexicana* line with a virulent, isogenic wild type precursor. We aim to identify key virulence factors and to explore the potential of the attenuated line as a vaccine candidate.

The current study has been conducted on promastigotes of *Leishmania mexicana* and it involves comparative multi-omics approaches to identify the molecules that contribute to Leishmania virulence. Log phase promastigotes of wild type and attenuated (H-line) were grown in parallel in media containing 10% FBS, and they were harvested for multi-omics analyses. For comparative proteomic analysis, protein extracts were labelled using 6-plex TMT and analyzed with LC-MS/MS. For metabolomics, metabolites were extracted with Chloroform/ Methanol/ Water (1:3:1) and analyzed with LC-MS. For transcriptomics, RNA was isolated and converted into a library of template molecules for cluster generation and DNA sequencing. We found twelve proteins differentially expressed in attenuated Leishmania (FC ≥1.5 and FDR ≤0.05) and 26 identified metabolites (FC ≥1.5 and FDR ≤0.05), whereas transcriptomics data found 67 transcripts that were differentially expressed (FC ≥2 and FDR ≤0.05). Correlation of these data reveals that the pentose phosphate pathway (PPP) and nucleotides (pyrimidine and purine) metabolism are significantly altered in attenuated Leishmania. Furthermore, a nucleobase and a biopterin transporter were significantly down regulated in proteomics analysis.

Notes:

31. Antimicrobial resistance genes: environmental impacts across landscapes in NE England and Scotland

Authors: Charles W. Knapp1, David W. Graham2, Yong-Guan Zhu3, Clare McCann2, Jian-Qiang Su3, Tanya Peshkur1, Martin Cooke2, Rupert Hough4, Thomas Freitag4, Lisa Avery4
Affiliation:
1. University of Strathclyde
2. Newcastle University
3. Chinese Academy of Sciences-Xiamen
4. James Hutton Institute

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Abstract:

Antimicrobial resistance is increasing in nature and threatens the effectiveness of our drug therapies and infection control. However, it remains difficult to distinguish what originates from human activities or what is natural. Therefore, we must extend the scale and depth of monitoring efforts to better understand what is driving the increases in resistance traits.

This project utilised two collections of previously characterised soils to compare and contrast distributions of AR genes under widely varying conditions, ranging from urban, agriculture, legacy mining, and pristine rural environments. From the soils, DNA were extracted and quantified for over 230 AR genes in each sample. These soil inventories provided us well-characterised soils and the wealth of information that describes both the soils and the impacts at source locations.

The project generated an astonishing 70,000 AR-related data points (300+ locations x 230 genes), each with extended background information on environmental conditions-creating among the largest geographic representation of AR gene distribution across landscapes ever created, sufficiently detailed to make cross-cutting observations of landscape effects on acquired vs innate AR levels.

Notes:

32. The dynamic picture of antimicrobial resistances in Campylobacter spp isolated from different host reservoirs in Scotland.

Authors: Bruno S. Lopes1 *, Norval J. C. Strachan2, Meenakshi Ramjee1, Anne Thomson1, Marion MacRae1 Sophie Shaw3 and Ken J. Forbes1
Affiliation:
[1]School of Medicine, Medical Sciences and Nutrition, University of Aberdeen, Foresterhill, Aberdeen, United Kingdom, AB25 2ZD.
[2]School of Biological Sciences, Cruickshank Building, University of Aberdeen, St. Machar Drive, Aberdeen, United Kingdom, AB24 3UU.
[3]Centre for Genome Enabled Biology and Medicine, 23. St Machar Drive, Old Aberdeen, AB24 3UU
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Abstract:

Campylobacter is the most common cause of bacterial gastroenteritis in Scotland with 5796 reported cases in 2017, a 9.1% increase compared to 2016. Our studies show that retail chicken plays a major role in the epidemiology of human cases of campylobacteriosis. The antibiotic resistance crisis not only makes effective treatment of severe foodborne infections difficult but also facilitates spread of resistances in different groups of bacteria. Hence, it is important to study the farm to fork transmission of resistant strains which may have a major impact on public health and economy. We analysed a total of 6689 *Campylobacter jejuni* and *C. coli* genomes associated with humans and other host reservoirs such as chicken, turkey, sheep, cattle, pigs and wild bird for resistance to four different classes of antibiotics. We found 29% (n=1962) had mutations conferring resistance to fluoroquinolones, 0.8% (n=59) had mutations associated with macrolide resistance, 32% (n= 2118) harboured a tetracycline resistance gene and 88% of isolates harboured a β-lactamase gene. ST5136, one of the most common strains in clinical infections, was also the most prevalent multi-drug resistant *C. jejuni* strain being resistant to at least four different classes of antimicrobials and was associated exclusively with poultry host reservoirs.

Notes:

33. A novel mecC allotype, mecC3, in a new staphylococcal species, Staphylococcus caeli

Authors: MacFadyen AC[1] and Paterson GK[1]
Affiliation: [1]Royal (Dick) School of Veterinary Studies and The Roslin Institute, University of Edinburgh, Easter Bush, Campus, Midlothian, EH25 9RG, UK.
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Abstract:

Methicillin-resistance in staphylococci is conferred by an alternative penicillin-binding protein (PBP2a/2') with low affinity for most β-lactam antibiotics. PBP2a is encoded by *mecA* which is carried on a mobile genetic element known as SCC*mec*. A variant of *mecA, mecC*, was described in 2011. *mecC* has been found in *Staphylococcus aureus* from humans and a wide range of animal species as well as a small number of other staphylococcal species. Integration into the chromosome by SCC*mec* is mediated by a group of serine recombinases, CcrAB and CcrC. Recently, we have identified a novel *mecC* allotype, *mecC3*, encoded by a new staphylococcal species, *Staphylococcus caeli,* 82B. We carried out genome sequencing to allow for an accurate assembly and comparative genomic study of the SCC*mec* region encoding *mecC3*. Not only is *mecC3* a novel allotype, it is also encoded within a SCC*mec* element distinct from those previously connected with *mecC*, which includes *ccrA5B3*, a previously unseen pairing associated with *mecC*, and *ccrC*.
The SCC*mec* element of *S. caeli* 82B, is dissimilar to the archetypal SCC*mec* XI encoding *mecC* in *S. aureus* and to other elements encoding *mecC,* which highlights the diverse context in which *mecC* may be found.

Notes:

34. Exploring Aurodox, A potential anti-virulence compound for the treatment of Escherichia coli infections of the gut.

Authors: Rebecca McHugh (1), Paul Hoskisson (1) and Andrew Roe (2)
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Abstract:

Anti-virulence compounds represent a novel solution for untreatable bacterial infections. These compounds typically prevent pathogenesis by inhibiting a single virulence factor without effect the growth of the infecting bacteria. Hence, they are less likely to exert selective pressures upon bacteria which lead to the evolution of resistance. Aurodox, a specialised metabolite of soil bacterium, Streptomyces goldiniensis, has recently been identified as an inhibitor of the Enteropathogenic Escherichia coli (EPEC) Type Three Secretion System (T3SS). In our initial studies, we have demonstrated the anti-virulence capacity of Aurodox by fully characterising its inhibitory effect on the T3SS of EPEC in addition to carriers of a homologous T3SS Enterohaemorrhagic Escherichia coli (EHEC) and Citrobacter rodentium. Through the use of RNA-seq transcriptome analysis, GFP-fusion reporter assays and tissue culture models, we have shown that Aurodox inhibits EHEC epithelial attachment at a transcriptional level, by downregulating the expression of Locus of Enterocyte Effacement (LEE) genes which encode for the T3SS. Currently, the production of Aurodox is difficult due to the low fermentation yield, resulting in high purchase costs. Therefore, we have used whole genome sequencing to identify the genes which encode for Aurodox production and have identified a putative Aurodox Biosynthetic Gene Cluster which we will therefore use to improve and diversify Aurodox production.

Notes:

35. Evaluation of antimicrobial resistance and biofilm formation of MRSA isolates from companion animals in Scotland

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Abstract:

Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major health threat in human and veterinary medicine causing infections without undergoing any host adaptation; ranging from mild skin infections to life-threatening bloodstream infections.
Veterinary clinical MRSA isolates from dogs and cats in Scotland were investigated for their susceptibility to oxacillin and fusidic acid and their ability to form biofilms. The aims were to determine whether isolates from certain body sites were better biofilm formers and whether sub-inhibitory antibiotic concentrations contributed to enhanced biofilm formation.
Oxacillin resistance was confirmed in all 27 MRSA isolates. Fusidic acid resistance was detected in four (15%) isolates. All isolates formed biofilms as measured by crystal violet assay. Strains isolated from nostrils were statistically better biofilm formers than isolates from other body sites. A trend of increased biofilm biomass when cultured in sub-inhibitory concentrations of oxacillin and fusidic acid was observed in 81% and 85% of isolates, respectively. The increased biofilm formation, however, was significant in two isolates (7%) for each antibiotic tested.
Overall, since animals have been suggested as antimicrobial resistance (AMR) reservoirs, this study emphasises the need for more intensive surveillance of antimicrobial resistance in animals and the role of biofilm formation in contributing to AMR maintenance.

Notes:

36. What are the trends in antimicrobial resistance patterns in bacteria isolated from companion animals in Scotland?

Authors: Ciaran McMonagle1, Willie Weir1 and Katarina Oravcova2
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Abstract:

Antimicrobial resistance (AMR) is one of the major health concerns facing the world in the coming years. Companion and production animals are thought to be a large reservoir of resistance genes with the capacity to transfer to humans through zoonotic infections and horizontal gene transfer. The intestinal microbiome of these animals is of interest as it harbours diverse microbes with pathogenic capacity.
This study analysed bacteriology data from the University of Glasgow's Veterinary Diagnostic Services with the aim to identify AMR trends between 2001 and 2016. A total of 31680 veterinary *Escherichia coli* isolates were investigated for the presence of phenotypic co-resistance patterns in 20 antimicrobial classes, with sulphonamides found to share the most resistances. In 13 of these classes over 90% of isolates harboured a co-resistance with sulphonamide, followed by high frequencies of co-resistance in isolates resistant to penicillins, aminoglycosides and tetracyclines.
A selection of 47 canine faecal and GIT *E. coli* isolates was tested for the presence of genetic determinants of its ESBL phenotype, with bla_{TEM} found to be the most prevalent (59%) and followed by $bla_{CTX\text{-}M}$ (6%). These genes are often present in human clinical ESBL strain, suggesting a shared pool of AMR genes and companion animals as a potential reservoir of AMR.

Notes:

37. The distribution of antibiotic resistance genes in fresh water in Scotland

Authors: Eulyn Pagaling, Joseph Palmer, Lisa Avery
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Abstract:

The National Waters Inventory for Scotland (NWIS) was developed by The James Hutton Institute to provide a national baseline study of the state of Scotland's water resource, which is required to understand resilience to the accumulating catchment pressures of delivering national objectives for food and renewable energy production, water supply for people, ecology and industry. This resource consists of waters sampled from primarily end-of-catchment sites. DNA was extracted from these waters, and screened for faecal indicator organisms, microbial diversity (via the 16S rRNA gene) and antibiotic resistance genes, including resistances to tetracycline (primarily animal usage) and β-latam (primarily human usage). This data was correlated to land use characteristics and other water characteristics. This research provides spatial and temporal distribution data of antibiotic resistance in Scotland.

Notes:

38. Antibody based biologics for treating bacterial and fungal infections

Authors: Soumya Palliyil1, Lily Fogg1, Sami Alawfi2, Sonia Gabriela Murillo Barrera2, Carol Munro2, Miguel Camara3, Andrew Porter1
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Abstract:

Within the Scottish Biologics Facility, we have developed a portfolio of monoclonal antibody based biologics for the early detection, diagnosis and treatment of bacterial and fungal infections. Three of our antimicrobial antibody projects will be showcased in the poster.

1. Immunomodulation of the quorum sensing signal molecules (QSSMs) of *Pseudomonas aeruginosa* by monoclonal antibodies (mAbs) as a novel approach to prevent *P. aeruginosa* infections
2. Using mAbs as tools for the early detection of QSSMs in bodily fluids as a possible first clue to an undiagnosed lung infection in Cystic Fibrosis patients
3. A new class of targeted and fungal specific mAbs for treating life-threatening Candida infections.

- Virulence factors help pathogens to invade the host, evade host defence mechanisms and establish disease. Antibodies are an attractive method of controlling bacterial virulence by, for example, blocking quorum sensing signalling as these 'anti-pathogenic' drugs are less likely to encourage the development of resistance in bacteria compared to conventional antibiotics.
- An immunoassay-based diagnostic system exploiting the high sensitivity of anti-QSSM mAbs could be developed to detect the presence of specific markers of *Pseudomonas* infection (homoserine lactones, quinolones) in bodily fluids such as blood and urine.
- The emergence of multi-drug resistant *Candida* species is a global concern and we have demonstrated the growth inhibitory activity of our anti-Candida antibodies using a multi-drug resistant strain.

Notes:

39. Applying the Mesolens to Microbiology - Visualising Biofilm Architecture and Substructure

Authors: Liam M. Rooney†1, Lee McCann2, Paul A. Hoskisson1 and Gail McConnell2
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Abstract:

Biofilms confer chemical and mechanical resistance to their constituent bacteria and facilitate the spread of antimicrobial resistance [1], establishing them as a focus of AMR research. Understanding the structure of biofilms is critical to developing novel methods of biofilm eradication. Previous studies show fractal-like spatial distributions of cells within biofilms resulting from cell-cell/cell-surface interactions [2, 3, 4]. However, their 3D architecture has largely been overlooked, perhaps limited by the capabilities of current imaging techniques where the size of the field of view is sacrificed for increased spatial resolution, or *vice versa*. Here we use the Mesolens, an optical microscope with a unique combination of low magnification (x4) and high numerical aperture (0.47) which has an imaging volume of 6x6x3 mm with a lateral resolution of 700 nm and an axial resolution of 7 μm [5]. The Mesolens allows imaging of whole live colony biofilms with sub-cellular resolution in a single dataset. We report intra-colony spatial structures (measuring ca.15 μm) which arise as an inherent property of biofilm formation in *Escherichia coli*. Observations of microbead translocation assays suggest that these features play a role in structural support and nutrient uptake. This finding contributes to fundamental principles of structural biology and bacterial community organisation.

Notes:

40. FBI Probe to Investigate Ivermectin Resistance in Nematodes

Authors: Stuart Ruddell, Prof Antony Page, Dr David France
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Abstract:

Parasitic nematodes (roundworms) are responsible for many diseases around the world. The World Health Organisation (WHO) estimates 1.5 billion people suffer from helminth (parasitic worm) infections.[1] In addition to human infection, parasitic nematodes represent significant pathogens in the agricultural industry. In the UK sheep industry, infestation with GI parasites costs an estimated £84 million per annum.[2]

Several anthelmintics are available to treat nematode infections, the most successful being the 16-membered macrocyclic lactone ivermectin (IVM). The importance of IVM is exemplified by its inclusion in the WHO List of Essential Medicines and its discovery earning the 2015 Nobel Prize for Medicine. Resistance to IVM is a global burden and pockets of IVM resistant nematodes are becoming increasingly numerous.[3] The mechanisms of resistance to IVM are currently unknown.

To investigate the primary mechanism of resistance, a fluorescent probe (FBI) (consisting of a bodipy fluorophore covalently attached to IVM) was synthesised and administered to *C. elegans*. FBI successfully determined the previously unknown uptake route of IVM to be amphidal. Furthermore, no probe was observed in resistant strains. These findings are consistent with our hypothesis that a primary mechanism of IVM resistance in nematodes is impaired drug uptake as a result of amphid dysfunction.

References:

[1] J. Bethony, *et al*., *Lancet*. **2006**, *367,* 1521
[2] G.J. Nieuwhof, S.C. Bishop, *Animal Science* **2005**, *81*, 23-29
[3] D. Yates, *et al*., *Int. J. Parasitol.* **2004**, *34*, 1075

Notes:

41. Are antimicrobial stewardship and sepsis awareness competing goals? A quantitative content analysis of UK national newspapers

Authors: Rush L (MBChB)[1], Patterson C[1], McDaid L[1], Hilton S[1].
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Abstract:

Background Antimicrobial resistance (AMR) is predicted to be responsible for ten million deaths globally every year by 2050. Reducing unnecessary prescribing is vital but may be complicated by a recent media focus on the need for earlier recognition and management of sepsis. This study is the first to compare how AMR and sepsis are represented in UK newspapers.

Methods Quantitative analysis of 458 articles about sepsis and antimicrobial resistance published in 11 UK national print newspapers between 30th January 1988 and 31st December 2016.

Findings AMR was framed as a global issue with multiple drivers and solutions impacting the future, whereas sepsis was presented as currently causing substantial mortality that is largely preventable through improved awareness. Few articles identified a need to balance timely management with the longer-term risks of overuse of antibiotics. Articles about sepsis contained personal narratives about affected individuals that were rare in articles about AMR.

Interpretation Lack of recognition of the relationship between sepsis and AMR is potentially damaging to promotion of rational prescribing and thus to ensuring availability of effective treatment for sepsis in the longer term. If emotive narratives about sepsis influence perceptions about the need for treatment they may negatively impact on efforts to promote reduced prescribing.

Funding UK Medical Research Council (MC_UU_12017/15 & (MC_UU_12017/11))/Scottish Government's Chief Scientist Office (SPHSU15 and SPHSU11).

Notes:

42. Characterisation of Inducible Antibiotic Production by Streptomycetes Isolated From Hyper-arid Environments

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Abstract:

The increase of antimicrobial resistance (AMR) is one of the biggest threats to human health. Current predictions estimate that by 2050 AMR will cause 10 million deaths. A major bottleneck is the high rediscovery rate of existing molecules and thus reduced discovery of novel bioactive compounds. One way to tackle this problem is to explore extreme environments in hope for identifying new unique metabolic pathways.

The lack of precipitation and high solar radiation makes the Atacama Desert in Chile the ultimate arid desert on Earth. This extreme environment is often compared to the conditions observed on Mars. Our main goal is the discovery and identification of novel secondary metabolites from the Atacama Desert.

Seventeen isolates from two distinct soil samples were identified using 16S rRNA as the same species, *Streptomyces phaeoluteigriseus* DSM 41896. Bioactivity assays using clinically relevant pathogens confirmed their potential for secondary metabolites production. Growth inhibition was observed against *Bacillus subtilis*, *Staphylococcus aureus* and *Enterococcus faecalis*.
These findings can lead to the identification of novel bioactive metabolites against some of the major threats to current human health.

We are currently investigating the potential for induction of some of these metabolites using a range of different salts.

Notes:

43. Analysis of the microbiome of wastewater and the prevalence of resistant Escherichia coli.

Authors: Tarteel Shuaib1, John Craft1, Colin Hunter2 and Janice Spencer1
Affiliation: School of Health and Life Science, Glasgow Caledonian University[1]; School of Engineering and Built Environment, Glasgow Caledonian University[2]
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Abstract:

Increasing environmental antimicrobial resistance (AMR) is an acknowledged major public health concern. Important in this rise is the prevalence of extended-spectrum β-lactamase (ESBL) Enterobacteriaceae . *Escherichia coli* carrying *bla*ESBL genes on plasmids are the most frequently isolated species producing ESBLs. Wastewater treatment plants have been suggested as hotsposts for emergence and dissemination of AMR. This study investigated the changes in the microbiome composition using 16S ribosomal sequencing at various points within an upgraded trickling filter wastewater treatment plant. The diversity and abundance of bacteria was significantly different at each sampling point with the diversity being higher in the influent than effluent . Forty three strains of *E. coli* were isolated at various points in the plant and the sensitivites to 18 antibiotics was investigated. Almost 50% of these isolates were resistant to at least one antibiotic and 26% were resitant to two or more antibiotics. 12 strains (28%) were found to be ESBL producing confirmed by the double disc test and PCR detecting ^{bla}TEM, ^{bla}SHV, and ^{bla}CTX-M. This data provides valuable insight into the composition of the microbiome of wastewater and the antimrcrobial resistance profile of *E. coli* isolated from wastewater.

Notes:

44. Bacterial Antibiotic Response in Micro-Environments

Authors: Daniel Taylor (Rosalind Allen, Simon Titmuss)
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Abstract:

A common method of quantitatively studying bacterial growth kinetics is through the use of a multiwell plate reader. This piece of equipment confines bacterial colonies in ~100µL "wells" whilst their growth kinetics are tracked over time using optical density measurements. It is currently unclear whether the growth kinetics of bacterial colonies grown in 100µL wells accurately mimics that of growth in-situ as clinical infections can occur in biological niches of much lower volume, such as those found in eukaryotic cell interiors or biofilms. In my research I have developed and tested a standalone microfluidic system that allows for the encapsulation of small bacterial colonies within microfluidic droplets of ~50µm radius. Each confined colony is independent from the next and 500-1000 droplets can be studied concurrently. This allows me to contrast the growth kinetics of bacterial colonies grown under antibiotic inhibition in a traditional multiwell plate, with those of bacterial colonies grown in spatial confinement comparable to that of an in-situ infection. Furthermore, it allows me to study large numbers of replicates simultaneously, allowing for statistically significant conclusions to be drawn from an inherently stochastic system.

Notes:

45. Co-selection of Antibiotic Resistance caused by a Legacy of PTE Pollution in Gram-Negative Bacteria

Authors: Rebecca Tonner1, Kiri Rodgers 2, Tanya Peshkur 1, Ian MacLellan2, Roderick Williams2, Andrew Hursthouse2, Fiona Henriquez2, Charles W. Knapp1*
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[2]*University of West of Scotland, Paisley UK*
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Abstract:

Antimicrobial resistant bacteria can become harboured in sediments of post-industrial estuaries. Subsequently, their resistance traits could be enriched by pollutants deposited in the sediments. Recent evidence strongly suggests this may pose hazards that not only affects the health care sector, but could also impact tourism and the aquaculture industries.

The River Clyde, UK was chosen for this study due to its extensive industrial history, and three sites were chosen to sample from representing different levels and types of industrial activities—two highly polluted and one relatively "pristine" site. We extracted and analysed for metal pollutants (or "potentially toxic elements", PTE), and other geochemical characteristics for all sediment cores. Gram-negative, enteric bacteria were isolated from all sediment cores from the three sites. Their susceptibilities to antibiotics and metals were assayed—determining minimum inhibitory concentrations (MIC) and minimum bactericidal concentrations (MBC).

The results indicate that co-selection of PTEs and antibiotic resistance does occur, and this impacts bacteria that are potential human pathogens. Higher concentrations of metals in the environment correlated to antibiotic resistance and higher MICs to metals than among bacteria found in less polluted sites.

To continue to protect human health, the interactions between environmental and human health must be fully understood. This study provides critical information behind the specific causes of antibiotic resistance due to a legacy of pollution.

Notes:

46. Estimates of antimicrobial usage on Scottish beef and dairy farms.

Authors: R.W. Humphry[1], M.K. Henry[1], A. Reeves[1], C. Correia-Gomes[1], G.J. Gunn[1], R. Smith[2], G. Innocent[3], S.C. Tongue[1]
Affiliation: [1] Epidemiology Research Unit (Inverness Campus), Scotland's Rural College (SRUC), King's Buildings, West Mains Road, Edinburgh EH9 3JG, U.K.
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[3] Biomathematics and Statistics Scotland, James Hutton Institute, Invergowrie, Dundee, DD2 5DA, U.K.
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Abstract:

The global focus on antimicrobial resistance has led to the usage of antimicrobials coming increasingly under scrutiny. Antimicrobial usage (AMU) in livestock production is one target area for improving antimicrobial stewardship. Consequently, livestock sector-specific targets for reduction in AMU have been introduced at UK level by the Responsible Use of Medicines in Agriculture (RUMA) Task Force. Estimates of on-farm AMU are required to establish baselines and set meaningful targets; in the absence of a mechanism to do this for the cattle sector, no such baselines exist. This study demonstrates the use of veterinary pharmaceutical sales data to estimate current AMU and to establish a baseline against which to judge future efforts to reduce AMU. Veterinary pharmaceutical sales data for 75 cattle farms (beef or dairy) from one Scottish veterinary practice database were used as a proxy estimate of on-farm AMU. The mean levels of sales to dairy farms were below the RUMA target for 2020; the mean levels of sales to beef farms were very slightly above the RUMA 2020 target. The outputs have provided initial estimates for this sector to Scottish Government and the Veterinary Medicines Directorate, on which to base policy development and further work in this area.

Notes:

47. Osteogenic and bactericidal properties of hydrothermal titania nanowires on titanium substrates

Authors: P.M. Tsimbouri1*, L. Fisher2, N. Holloway3 , T. Sjostrom2, A.H. Nobbs2, R.M.D Meek4, B. Su2, M.J. Dalby1
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[2] School of Oral and Dental Sciences, University of Bristol, Bristol, UK
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Abstract:

Nanotopographical cues on Ti have been shown to support cell differentiation and selective growth. Bone remodelling is a constant process and the use of nanotopographical features to promote cell adhesion and bone formation is hoped to improve osteointegration and clinical outcomes. Furthermore, infection by biofilm formation on surgical implants is a major issue. Our aim is to identify nanotopographies on Ti surfaces that would be optimal for both bone remodelling and for reducing risk of bacterial infection. Primary human osteoblast/osteoclast co-cultures were seeded onto Ti substrates with TiO_2 nanowires formed under alkaline conditions at 240 ^{o}C for different times (2, 2.5 or 3 h). Cell growth and behaviour was assessed by immunofluorescence microscopy, histochemistry, SEM and quantitative RT-PCR methods. Bacterial growth on the nanowire surfaces was assessed by confocal microscopy and SEM. From the three surfaces tested the 2h nanowire surface supported osteoblast and to a lesser extent osteoclast growth and differentiation. At the same time bacterial viability was reduced to 60% on the 2h nanowires. Hence the 2h surface provided optimal bone remodeling in *in vitro* conditions while reducing infection risk, making it a favourable candidate for future implant surfaces. This work was funded by EPSRC grant EP/K034898/1.

Notes:

48. Heavy Metal Inducible Antimicrobial Activity of Streptomyces spp. Isolated from the Leadhills and Wanlockhead Lead Mines in Scotland.

Authors: Talal Salih1, Leena Nieminen1, Alison MacFadyen2, Nicholas Tucker1*
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Abstract:

There is a real and urgent need for new antibiotics to combat the rise of antibiotic resistance. There are also an increasing number of reports that correlate resistance to heavy metals with antibiotic resistance. It has also been shown that triggering the expression of cryptic gene clusters in *Streptomyces* might yield novel antibiotics. Here, we isolated Streptomyces strains from sediments contaminated with heavy metals from a former industrial site in Scotland and these strains were assayed for heavy metal dependent antimicrobial activity. We have used a combination genomics and transcriptomics to investigate these novel strains, providing a phylogenetic context and molecular evidence towards the discovery of the gene clusters responsible for antibiotic biosynthesis. Our findings highlight the potential of using heavy metals for activation of silent secondary metabolite gene clusters in Streptomyces isolated from extreme environments for natural product discovery. These findings are supported by the fact that these compounds are produced only in presence of sub-inhibitory concentrations of heavy metals but not in the absence of metal induction. Whole genome sequencing has enabled us to investigate the taxonomy and biosynthetic capacity of the strains whilst transcriptomic and metabolomic analyses are allowing us to investigate the changes that occur under metal-inducing conditions.

Keywords: Streptomyces, heavy metal, antibiotic induction

Notes:

49. Genes of past, present and future: does legacy pollution contribute to antibiotic resistance in industrialised estuaries?

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Abstract:

The legacy of past pollution exists in many estuaries of industrialised cities. Persistent pollutants, historically discharged into waterways, have become incorporated into sediment layers as a record of past, unregulated release. Preliminary reports have shown that pollution legacies have the potential of affecting antimicrobial resistance (AMR) in exposed bacteria. The sediment zones become reactors with the biochemical stressors to stimulate the production and dissemination of AR genes. By co-selection processes the genes could simultaneously select for genes for antibiotic resistance. Herein, we report evidence of the emergence of AMR is sediment cores of the Clyde Estuary.

Notes:

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